

OIPE

## RAW SEQUENCE LISTING

DATE: 08/08/2001

PATENT APPLICATION: US/09/919,585

TIME: 11:44:01

Input Set : A:\PTO\_VSK.txt

Output Set: N:\CRF3\08082001\I919585.raw

ENTERED

4 &lt;110&gt; APPLICANT: Sun, Tian-Qiang

5 Feng, Jia-Jia

6 Reinhard, Christoph

7 Fantl, Wendy J.

8 Williams, Lewis T.

11 <120> TITLE OF INVENTION: ISOLATION OF DROSOPHILA AND HUMAN POLYNUCLEOTIDES ENCODING  
PAR-1 KINASE,

12 POLYPEPTIDES ENCODED BY THE POLYNUCLEOTIDES AND METHODS UTILIZING THE

13 POLYNUCLEOTIDES AND POLYPEPTIDES

16 &lt;130&gt; FILE REFERENCE: PP-016093.002/200130.525

OK--&gt; 18 &lt;140&gt; CURRENT APPLICATION NUMBER: US/09/919,585 OK

19 &lt;141&gt; CURRENT FILING DATE: 2001-07-30

21 &lt;160&gt; NUMBER OF SEQ ID NOS: 22

23 &lt;170&gt; SOFTWARE: FastSEQ for Windows Version 4.0

25 &lt;210&gt; SEQ ID NO: 1

26 &lt;211&gt; LENGTH: 2271

27 &lt;212&gt; TYPE: DNA

28 &lt;213&gt; ORGANISM: Homo sapiens

30 &lt;400&gt; SEQUENCE: 1

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39	gcaagatcta	aatttagaca	gattgtgtct	gcagttcaat	actgccatca	gaaacggatc	540
40	gtacatcgag	acctcaaggc	tgaaaatcta	ttgttagatg	ccgatatgaa	cattaaaata	600
41	gcagatttcg	gttttagcaa	tgaatttact	gttggcggta	aactcgacac	gttttgtggc	660
42	agtcctccat	acgcagcacc	tgagctcttc	cagggcaaga	aatatgacgg	gccagaagtg	720
43	gatgtgtgga	gtctgggggt	cattttatac	acactagtca	gtggctcact	tccttttgat	780
44	gggcaaaacc	taaaggaact	gagagagaga	gtattaagag	ggaaatacac	aattcccttc	840
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46	cgcggcactc	tagagcaaat	catgaaggac	aggtggatca	atgcagggca	tgaagaagat	960
47	gaactcaaac	catttggtga	accagagcta	gacatctcag	acaaaaaaag	aatagatatt	1020
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50	gattccagtt	ctagcagcaa	tctttcactt	gctaaggtta	ggccgagcag	tgatctcaac	1200
51	aacagtactg	gccagtctcc	tcaccacaaa	gtgcagagaa	gtgtttcttc	aagccaaaag	1260
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56	agtaacacag	catctggtgg	aatgacacga	cgaaatactt	atgtttgcag	tgagagaact	1560
57	acagctgata	gacactcagt	gattcagaat	ggcaaagaaa	acagcactat	tcctgatcag	1620
58	agaactccag	ttgcttcaac	acacagtatc	agtagtgac	ccaccccgaa	tcgaatccgc	1680
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62 aggcttccaa ctgaatatga gaggaacggg agatatgagg gctcaagtcg caatgtatct 1920
63 gctgagcaaa aagatgaaaa caaagaagca aagcctcgat ccctacgctt cacctggagc 1980
64 atgaaaacca ctagtccaat ggatcccggg gacatgatgc gggaaatccg caaagtgttg 2040
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67 tctctgaacg gggctccggtt taagcgggata tcgggggacat ccatagcctt caaaaaatatt 2220
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73 <213> ORGANISM: Homo sapiens
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79 ttgatgtctg acaacttttg ttagccgttc cccttaaaac gttttcattt taaccgttct 240
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83 cgttcacctc cacttcataa actgataaac caacgtgtac cgtcctactt cctttttctt 480
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87 tcaggaggta tgcgtcgtgg actcgagaag gtcccgctct ttatactgcc cggctctcac 720
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109 tacttttggg gatcaagtta cctaggggcc ctgtactacg cccttttaggc gtttcacaac 2040
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111 ctacccgtgc gcctcttgga gcacgtcacc ctttaccttc acacgttcga cggttctgac 2160
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116 <211> LENGTH: 744
117 <212> TYPE: PRT
118 <213> ORGANISM: Homo sapiens
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123 Asn His Thr Ser His Gly Asp Gly Arg Gln Glu Val Thr Ser Arg Thr
124 20 25 30
125 Ser Arg Ser Gly Ala Arg Cys Arg Asn Ser Ile Ala Ser Cys Ala Asp
126 35 40 45
127 Glu Gln Pro His Ile Gly Asn Tyr Arg Leu Leu Lys Thr Ile Gly Lys
128 50 55 60
129 Gly Asn Phe Ala Lys Val Lys Leu Ala Arg His Ile Leu Thr Gly Arg
130 65 70 75 80
131 Glu Val Ala Ile Lys Ile Ile Asp Lys Thr Gln Leu Asn Pro Thr Ser
132 85 90 95
133 Leu Gln Lys Leu Phe Arg Glu Val Arg Ile Met Lys Ile Leu Asn His
134 100 105 110
135 Pro Asn Ile Val Lys Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu
136 115 120 125
137 Tyr Leu Ile Met Glu Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu
138 130 135 140
139 Val Ala His Gly Arg Met Lys Glu Lys Glu Ala Arg Ser Lys Phe Arg
140 145 150 155 160
141 Gln Ile Val Ser Ala Val Gln Tyr Cys His Gln Lys Arg Ile Val His
142 165 170 175
143 Arg Asp Leu Lys Ala Glu Asn Leu Leu Leu Asp Ala Asp Met Asn Ile
144 180 185 190
145 Lys Ile Ala Asp Phe Gly Phe Ser Asn Glu Phe Thr Val Gly Gly Lys
146 195 200 205
147 Leu Asp Thr Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe
148 210 215 220
149 Gln Gly Lys Lys Tyr Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly
150 225 230 235 240
151 Val Ile Leu Tyr Thr Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln
152 245 250 255
153 Asn Leu Lys Glu Leu Arg Glu Arg Val Leu Arg Gly Lys Tyr Arg Ile
154 260 265 270
155 Pro Phe Tyr Met Ser Thr Asp Cys Glu Asn Leu Leu Lys Arg Phe Leu
156 275 280 285
157 Val Leu Asn Pro Ile Lys Arg Gly Thr Leu Glu Gln Ile Met Lys Asp
158 290 295 300
159 Arg Trp Ile Asn Ala Gly His Glu Glu Asp Glu Leu Lys Pro Phe Val
160 305 310 315 320
161 Glu Pro Glu Leu Asp Ile Ser Asp Gln Lys Arg Ile Asp Ile Met Val

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163 Gly Met Gly Tyr Ser Gln Glu Glu Ile Gln Glu Ser Leu Ser Lys Met
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165 Lys Tyr Asp Glu Ile Thr Ala Thr Tyr Leu Leu Leu Gly Arg Lys Ser
166          355          360          365
167 Ser Glu Leu Asp Ala Ser Asp Ser Ser Ser Ser Asn Leu Ser Leu
168          370          375          380
169 Ala Lys Val Arg Pro Ser Ser Asp Leu Asn Asn Ser Thr Gly Gln Ser
170 385          390          395          400
171 Pro His His Lys Val Gln Arg Ser Val Ser Ser Ser Gln Lys Gln Arg
172          405          410          415
173 Arg Tyr Ser Asp His Ala Gly Pro Ala Ile Pro Ser Val Val Ala Tyr
174          420          425          430
175 Pro Lys Arg Ser Gln Thr Ser Thr Ala Asp Ser Asp Leu Lys Glu Asp
176          435          440          445
177 Gly Ile Ser Ser Arg Lys Ser Ser Gly Ser Ala Val Gly Gly Lys Gly
178          450          455          460
179 Ile Ala Pro Ala Ser Pro Met Leu Gly Asn Ala Ser Asn Pro Asn Lys
180 465          470          475          480
181 Ala Asp Ile Pro Glu Arg Lys Lys Ser Ser Thr Val Pro Ser Ser Asn
182          485          490          495
183 Thr Ala Ser Gly Gly Met Thr Arg Arg Asn Thr Tyr Val Cys Ser Glu
184          500          505          510
185 Arg Thr Thr Ala Asp Arg His Ser Val Ile Gln Asn Gly Lys Glu Asn
186          515          520          525
187 Ser Thr Ile Pro Asp Gln Arg Thr Pro Val Ala Ser Thr His Ser Ile
188          530          535          540
189 Ser Ser Ala Ala Thr Pro Asp Arg Ile Arg Phe Pro Arg Gly Thr Ala
190 545          550          555          560
191 Ser Arg Ser Thr Phe His Gly Gln Pro Arg Glu Arg Arg Thr Ala Thr
192          565          570          575
193 Tyr Asn Gly Pro Pro Ala Ser Pro Ser Leu Ser His Glu Ala Thr Pro
194          580          585          590
195 Leu Ser Gln Thr Arg Ser Arg Gly Ser Thr Asn Leu Phe Ser Lys Leu
196          595          600          605
197 Thr Ser Lys Leu Thr Arg Arg Leu Pro Thr Glu Tyr Glu Arg Asn Gly
198          610          615          620
199 Arg Tyr Glu Gly Ser Ser Arg Asn Val Ser Ala Glu Gln Lys Asp Glu
200 625          630          635          640
201 Asn Lys Glu Ala Lys Pro Arg Ser Leu Arg Phe Thr Trp Ser Met Lys
202          645          650          655
203 Thr Thr Ser Ser Met Asp Pro Gly Asp Met Met Arg Glu Ile Arg Lys
204          660          665          670
205 Val Leu Asp Ala Asn Asn Cys Asp Tyr Glu Gln Arg Glu Arg Phe Leu
206          675          680          685
207 Leu Phe Cys Val His Gly Asp Gly His Ala Glu Asn Leu Val Gln Trp
208          690          695          700
209 Glu Met Glu Val Cys Lys Leu Pro Arg Leu Ser Leu Asn Gly Val Arg
210 705          710          715          720

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213 Lys Ile Ala Asn Glu Leu Lys Leu ✓
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217 <211> LENGTH: 2112
218 <212> TYPE: DNA
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224 aagttggccc gacacatcct gactgggaaa gaggtagctg tgaagatcat tgacaagact      180
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260 <211> LENGTH: 2112
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens

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L:18 M:270 C: Current Application Number differs, Wrong Format